

09/646679

-1-

534 Rec'd PCT/PTG 20 SEP 2000  
SEQUENCE LISTING

<110> Wyatt, Paul  
Roberts, Jeremy A.  
Whitelaw, Catherine

<120> Signal Transduction Protein Involved in Plant Dehiscence

<130> 0623.0890000

<140> To Be Assigned

<141> Herewith

<150> GB9806113.8

<151> 1998-03-20

<160> 38

<170> PatentIn Ver. 2.0

<210> 1

<211> 14

<212> DNA

<213> Artificial Sequence

<220>

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14

<210> 2

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10

<210> 3

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PatentIn Ver. 2.0



<211> 27  
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27

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<223> Description of Artificial Sequence: Primer DZ2FLA

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28

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28

<210> 11  
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22

<210> 12  
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<400> 12  
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<400> 13  
ggcctgcagt gcctaggatc tggaagc 27

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<211> 605  
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<222> (20)..(427)

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1 5 10

ata aag aag aaa cta aac gtg ttg atc gtc gat gat gat cca cta aac 100  
Ile Lys Lys Lys Leu Asn Val Leu Ile Val Asp Asp Asp Pro Leu Asn  
15 20 25

ctt ata att cat gag aag atc atc aaa gcg att ggg ggt att tca cag 148  
Leu Ile Ile His Glu Lys Ile Ile Lys Ala Ile Gly Gly Ile Ser Gln  
30 35 40

aca gcg aat aac ggt gag gag gca gta atc atc cac cgt gac ggc ggc 196  
Thr Ala Asn Asn Gly Glu Glu Ala Val Ile Ile His Arg Asp Gly Gly  
45 50 55

tca tct ttt gac ctt atc cta atg gat aaa gaa atg ccc gag agg gat 244  
Ser Ser Phe Asp Leu Ile Leu Met Asp Lys Glu Met Pro Glu Arg Asp  
60 65 70 75

ggg gtt tcg aca act aag aag cta aga gaa atg gaa gtg aag tca atg 292  
Gly Val Ser Thr Thr Lys Lys Leu Arg Glu Met Glu Val Lys Ser Met  
80 85 90

att gtt ggg gtg act tca ctg gct gac aat gaa gag gag cgc agg gct 340  
Ile Val Gly Val Thr Ser Leu Ala Asp Asn Glu Glu Glu Arg Arg Ala  
95 100 105

64954950

ttc atg gaa gct gga ctt aac cat tgc ttg gca aaa ccg tta acc aag 388  
Phe Met Glu Ala Gly Leu Asn His Cys Leu Ala Lys Pro Leu Thr Lys  
110 115 120

gac aag atc atc cct ctc att aac caa ctc atg gat gct tgatggatat 437  
Asp Lys Ile Ile Pro Leu Ile Asn Gln Leu Met Asp Ala  
125 130 135

atattttata ttatggaaac acacataata acgtctaagt gtgtatgtat gcatagatac 497

ttgcatgtgt gtgttttaga atttaggggtt ctttatcgtc cgtgatatat aatcatgtaa 557

gttggttgctt taagcttata aaatatttaa ataagggttt cctctacc 605

<210> 15  
<211> 136  
<212> PRT  
<213> Brassica napus

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1 5 10 15

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20 25 30

Lys Ile Ile Lys Ala Ile Gly Gly Ile Ser Gln Thr Ala Asn Asn Gly  
35 40 45

Glu Glu Ala Val Ile Ile His Arg Asp Gly Gly Ser Ser Phe Asp Leu  
50 55 60

Ile Leu Met Asp Lys Glu Met Pro Glu Arg Asp Gly Val Ser Thr Thr  
65 70 75 80

Lys Lys Leu Arg Glu Met Glu Val Lys Ser Met Ile Val Gly Val Thr  
85 90 95

Ser Leu Ala Asp Asn Glu Glu Glu Arg Arg Ala Phe Met Glu Ala Gly  
100 105 110

Leu Asn His Cys Leu Ala Lys Pro Leu Thr Lys Asp Lys Ile Ile Pro  
115 120 125

Leu Ile Asn Gln Leu Met Asp Ala  
130 135

<210> 16  
<211> 136  
<212> PRT  
<213> Brassica napus

<400> 16

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Ser Lys Thr Pro Asp Val Leu Leu Ser Asp Ile Arg Met Pro Gly Met  
50 55 60

His Tyr Gln Glu Gln Gln Gln Pro Arg Asn Ile Glu Val Asn Gly Pro  
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<212> PRT
<213> Bacillus subtilis
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20 25 30

Ala Ala Asn Gly Leu Gln Ala Leu Asp Ile Val Thr Lys Glu Arg Pro  
35 40 45

Asp Leu Val Leu Leu Asp Met Lys Ile Pro Gly Met Asp Gly Ile Glu  
50 55 60

Ile Leu Lys Arg Met Lys Val Ile Asp Glu Asn Ile Arg Val Ile Ile  
65 70 75 80

Met Thr Ala Tyr Gly Glu Leu Asp Met Ile Gln Glu Ser Lys Glu Leu  
85 90 95

Gly Ala Leu Thr His Phe Ala Lys Pro Phe Asp Ile Asp Glu Ile Arg  
100 105 110

Asp Ala Val Lys Lys Tyr Leu Pro Leu Lys Ser Asn  
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<210> 21
<211> 129
<212> PRT
<213> Escherichia coli
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<210> 22
<211> 111
<212> PRT
<213> Arabidopsis thaliana

<220>
<221> Unsure
<222> 67
<223> Xaa= any amino acid
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Lys Gly Leu Leu Val His Leu Gly Cys Glu Val Thr Thr Val Ser Ser
          20                      25                      30
Asn Glu Glu Cys Leu Arg Val Val Ser His Glu His Lys Val Val Phe
          35                      40                      45
Met Asp Val Cys Met Pro Gly Val Glu Asn Tyr Gln Ile Ala Leu Arg
  50                      55                      60
Ile His Xaa Pro Leu Leu Val Ala Leu Ser Gly Asn Thr Asp Lys Ser
  65                      70                      75                      80
Thr Lys Glu Lys Cys Met Ser Phe Gly Leu Asp Gly Val Leu Leu Lys
          85                      90                      95

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Pro Val Ser Leu Asp Asn Ile Arg Asp Val Leu Ser Asp Leu Leu  
100 105 110

<210> 23  
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<212> DNA  
<213> Brassica napus

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<222> (1516)..(1716)

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T. 6251960

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caaaaaaaaaa aaaaacnttt tataatntcaa ctatgagcaa ttattctttat agtggttttct 180
ttttccagaa atttgacgac aacctaacta aaacaattta atttgacggt agttaagtaa 240
tttatataga tggataaatt gagcaagcac attacgaact gcggatcaag gagagtcaca 300
atttaattct tacgtttatac acaaaattat ctaaatacta tatatatata cagctgcatg 360
ctacgataat gatcaaagt ttatgtactt ttcagcgaaa attcttgtcg ccatacatta 420
ctgtgttaaat gaatcattaa atatgtgaag gaggaaaaga gtacaaaagg agttttgttg 480
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aggcatttcg	cagacactga	aatgtgaata	ataataaag	aattgccgaa	ttgatttcta		540
gttggtgaag	tgggtgaaaa	ttgtatgtcc	attgcttata	aactataaaa	tataatatnt		600
tnatattatc	actntggaca	ttagtningat	agaccctagc	taaaattttt	aaaaattata		660
cattcatttt	ctnaagtacc	aaacttaatt	atcaccaatcg	gataaaattg	tttaagaaac		720
cattacaaac	tcagcttgtg	gactctgaga	gaaactaaga	gctagacata	cggtttagtag		780
tgtagccgca	tttttttatgc	ttaatttgct	taagcatgac	ttctatgctc	cttgatgata		840
tttatttttaa	tatcctagga	catatggatt	tgataaagat	cttatcaacc	tttcaacaag		900
accatttagct	caacaaacaa	aatactgaaa	gtatataatc	ttggttacag	aattccttatg		960
ccaaaaatat	cataatatat	atagaattcg	gttatgatta	agatgaatta	tttaattaat		1020
atattttttca	cttttgTTTT	cttatgtatt	cttagtattt	gttcaccata	ttgaccgatt		1080
ggtgtcatat	tagtttggtg	agacaactca	gttgcaacga	tgcagattac	atttcaggaa		1140
gattcatgta	agaaagatat	ttcgctttgt	ggtgtgaaaa	tatgcctctt	tcactttttt		1200
tcaactataa	atttcgatcg	atgtatctac	gttctttaaca	caattcacaa	tcttcttttag		1260
aatccaaaat	tgtaagccgc	tttctaattct	ctttctcagt	atacatatgt	aatatgtatg		1320
catatattat	tattcataat	acaaacacga	acctatgcat	gcaagaagat	agttacacgc		1380
tcataacaaa	cacaaaaaaaa	catacgcatg	cattagaaca	cttgtatgtt	aatttccata		1440
atgtttttgca	taaacattct	tcgttttaat	tagcttcttt	ttgtgtgaag	attgttcgaa		1500
gaaaaaaaaac	cgaag atg gca aca acg tca aca tcc acg gga gat atc aag						1551
	Met Ala Thr Thr Ser Thr Ser Thr Gly Asp Ile Lys						
	1                    5                    10						
aaa acc aag tca gta gaa gtg aag aag aaa ctt aac gtg ttg atc gtt							1599
Lys Thr Lys Ser Val Glu Val Lys Lys Lys Leu Asn Val Leu Ile Val							
	15                    20                    25						
gat gat gat aca gta att cgt aaa ctt cac gag aat atc atc aaa tcg							1647
Asp Asp Asp Thr Val Ile Arg Lys Leu His Glu Asn Ile Ile Lys Ser							
	30                    35                    40						
atc ggt gga att tca cag acg gct aag aac ggt gag gag gca gtg aac							1695
Ile Gly Gly Ile Ser Gln Thr Ala Lys Asn Gly Glu Glu Ala Val Asn							
	45                    50                    55                    60						
atc cac cgc gac ggc aat gca							1716
Ile His Arg Asp Gly Asn Ala							
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<210> 24  
<211> 67  
<212> PRT  
<213> Brassica napus

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20 25 30  
Val Ile Arg Lys Leu His Glu Asn Ile Ile Lys Ser Ile Gly Gly Ile  
35 40 45  
Ser Gln Thr Ala Lys Asn Gly Glu Glu Ala Val Asn Ile His Arg Asp  
50 55 60  
Gly Asn Ala  
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catctttcga ccttatccta atggataaag aaatgccga gagggatgga ctttcggcaa 180  
ctaagaagct aagagaaatg aaagtgacgt ctatgattat tggggtgacg aactggctg 240  
acaatgaaga ggaacgtaag gctttcatgg aagctggact taaccattgc ttggcaaac 300  
ccttaagcaa agccaagatc ctccctctca tcaacaatct catggatgct tgatggatgg 360  
atgaattgtc gccactacat atctacatta tacaatatg aaaaacacat ataataacgt 420  
catacacctg tgtgtgtatg catagatatc tatccgcattg tgtgttttta gggttgttat 480  
gtttgatttt tattgtgcgt ggcgtgatat acaatcangt nagtcgttac ttttggctta 540

taaaataatg aataagattt gttaaaaata aaaaaa

576

<210> 26  
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<212> PRT  
<213> Brassica napus

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<223> Xaa= any amino acid

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Ser Ile Gly Gly Ile Ser Gln Thr Ala Lys Asn Gly Glu Glu Ala Val  
20 25 30  
Asn Ile His Arg Asp Gly Asn Ala Ser Phe Asp Leu Ile Leu Met Asp  
35 40 45  
Lys Glu Met Pro Glu Arg Asp Gly Leu Ser Ala Thr Lys Lys Leu Arg  
50 55 60  
Glu Met Lys Val Thr Ser Met Ile Ile Gly Val Thr Thr Leu Ala Asp  
65 70 75 80  
Asn Glu Glu Glu Arg Lys Ala Phe Met Glu Ala Gly Leu Asn His Cys  
85 90 95  
Leu Ala Lys Pro Leu Ser Lys Ala Lys Ile Leu Pro Leu Ile Asn Asn  
100 105 110  
Leu Met Asp Ala  
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<210> 27  
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<223> Xaa= any amino acid

<400> 27

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tcattttttaa cttacttctt tttttttggt gaagattctt gagagaaaag aaatcgaag 179

atg gca aca aaa tcc acc gga ggt acc gag aaa acc aag tcg ata gaa 227
Met Ala Thr Lys Ser Thr Gly Gly Thr Glu Lys Thr Lys Ser Ile Glu
  1             5             10             15

gtg aag aag aaa cta atc aac gtg ttg atc gtc gat gat gat cca tta 275
Val Lys Lys Lys Leu Ile Asn Val Leu Ile Val Asp Asp Asp Pro Leu
          20             25             30

aac cgt aga ctc cac gag atg atc atc aaa acg atc gga gga att tct 323
Asn Arg Arg Leu His Glu Met Ile Ile Lys Thr Ile Gly Gly Ile Ser
          35             40             45

cag act gca aag aat ggc gaa gag gcn gtg atc ctc cac cgt gac ggc 371
Gln Thr Ala Lys Asn Gly Glu Glu Xaa Val Ile Leu His Arg Asp Gly
          50             55             60

gaa gca tct ttc gac ctt att cta atg gat aag gaa atg cct gag agg 419
Glu Ala Ser Phe Asp Leu Ile Leu Met Asp Lys Glu Met Pro Glu Arg
          65             70             75             80

gat gga gtt tcg aca att aag ang cta aga gaa atg aaa ggg acg tca 467
Asp Gly Val Ser Thr Ile Lys Xaa Leu Arg Glu Met Lys Gly Thr Ser
          85             90             95

atg atc gtt ggg gta acg tca gta gct gac caa gaa gaa gag cgt aag 515
Met Ile Val Gly Val Thr Ser Val Ala Asp Gln Glu Glu Arg Lys
          100             105             110

gct ttt atg gaa gct ggg ctc aac cat tgc ttg gaa aaa ccc tta acc 563
Ala Phe Met Glu Ala Gly Leu Asn His Cys Leu Glu Lys Pro Leu Thr
          115             120             125

aag gcc aag atc ttc ccg ctc att agc cac ctc ttc gat gct 605
Lys Ala Lys Ile Phe Pro Leu Ile Ser His Leu Phe Asp Ala
          130             135             140

tgatggatga aggctcatta atgtatctat attttcaatc atgaaatcac ctacacgtgt 665

atttgacaca aaaatctgca tttgttgtga tatagggttt ctcatatcta tgtttgattt 725

attttcttat cgtccgaggt aaaatcatgc aagtcatttc ttttggctaa taaaatatta 785

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                   20                  25                  30  
 Asn Arg Arg Leu His Glu Met Ile Ile Lys Thr Ile Gly Gly Ile Ser  
           35                  40                  45  
 Gln Thr Ala Lys Asn Gly Glu Glu Xaa Val Ile Leu His Arg Asp Gly  
           50                  55                  60  
 Glu Ala Ser Phe Asp Leu Ile Leu Met Asp Lys Glu Met Pro Glu Arg  
           65                  70                  75                  80  
 Asp Gly Val Ser Thr Ile Lys Xaa Leu Arg Glu Met Lys Gly Thr Ser  
                   85                  90                  95  
 Met Ile Val Gly Val Thr Ser Val Ala Asp Gln Glu Glu Glu Arg Lys  
           100                  105                  110  
 Ala Phe Met Glu Ala Gly Leu Asn His Cys Leu Glu Lys Pro Leu Thr  
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actgttgaaa aactaatgct ctataaaaca ctagacaata acaaaaatacg taatgcgtaa 300

tcataqtaaa qcattacqaa tacqacattg aacactactg acatataaag tagtagattt 420

tacttcatga gaatatcct cgttctatac tagcagaagg gttcgatagt gattttacaa 540

tacatttctt gtctaaatta tcaaataaca tactctcttt tgtttactta taaacgatat 660

aatatatata tattttttttt catttctact catgtttctt atacattctt taaatttggt 780

agattacatt tcagccaaat tcatgtaaaa gatgcttttc tttgtgatgt ttttaaaatg 900

gaacataaga tcttctttaa aatccaaaat cgtaggccac tatttcatta tacttatgta 1020

tgatcacaca cgcacacaca tagaaacata aacacgcaat aattttctata cagttttaatt 1140

atg gca aca aaa tcc acc gga ggt acc gag aaa acc aag tcg ata gaa 1247

1                      5                      10                      15

Val Lys Lys Lys Leu Ile Asn Val Leu Ile Val Asp Asp Asp Pro Leu

20 25 30

Asn Arg Arg Leu His Glu Cys His Gln

35 40

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Val Lys Lys Lys Leu Ile Asn Val Leu Ile Val Asp Asp Asp Pro Leu
          20             25             30
Asn Arg Arg Leu His Glu Cys His Gln
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aagattagcg	tttcaaaccc	cgaa	atg	gcc	cgt	tgt	cat	gga	agt	ctt	gct	171						
			Met	Ala	Arg	Cys	His	Gly	Ser	Leu	Ala							
			1					5										
att	ttc	tta	tgc	gtt	ctt	ttg	atg	ctc	gct	tgc	tgc	caa	gct	ttg	agt	219		
Ile	Phe	Leu	Cys	Val	Leu	Leu	Met	Leu	Ala	Cys	Cys	Gln	Ala	Leu	Ser			
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agc	aac	gta	gat	gat	gga	tat	ggt	cat	gaa	gat	gga	agc	ttc	gaa	acc	267		
Ser	Asn	Val	Asp	Asp	Gly	Tyr	Gly	His	Glu	Asp	Gly	Ser	Phe	Glu	Thr			
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gat	agt	tta	atc	aag	ctc	aac	aac	gac	gac	gac	gtt	ctt	acc	ttg	aaa	315		
Asp	Ser	Leu	Ile	Lys	Leu	Asn	Asn	Asp	Asp	Asp	Val	Leu	Thr	Leu	Lys			
			45					50					55					
agc	tcc	gat	aga	ccc	act	acc	gaa	tca	tca	act	gtt	agt	gtt	tcg	aac	363		
Ser	Ser	Asp	Arg	Pro	Thr	Thr	Glu	Ser	Ser	Thr	Val	Ser	Val	Ser	Asn			
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ttc	gga	gca	aaa	ggt	gat	gga	aaa	acc	gat	gat	act	cag	gct	ttc	aag	411		
Phe	Gly	Ala	Lys	Gly	Asp	Gly	Lys	Thr	Asp	Asp	Thr	Gln	Ala	Phe	Lys			
	75					80					85							
aaa	gca	tgg	aag	aag	gca	tgt	tca	aca	aat	gga	gtg	act	act	ttc	ttg	459		

Lys 90	Ala	Trp	Lys	Lys	Ala 95	Cys	Ser	Thr	Asn	Gly 100	Val	Thr	Thr	Phe	Leu 105	
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cca Pro	tgc Cys	aaa Lys	tca Ser 125	tta Leu	cgt Arg	agc Ser	ttc Phe	cag Gln 130	atc Ile	cta Leu	ggc Gly	act Thr 135	tta Leu	tca Ser	gct Ala	555
tct Ser	aca Thr	aaa Lys 140	cga Arg	tcg Ser	gat Asp	tac Tyr	agt Ser 145	aat Asn	gac Asp	aag Lys	aac Asn 150	cac His	tgg Trp	ctt Leu	att Ile	603
ttg Leu	gag Glu 155	gac Asp	gtt Val	aat Asn	aat Asn 160	cta Leu	tca Ser	atc Ile	gat Asp	ggc Gly 165	ggc Gly	tcg Ser	gcg Ala	ggg Gly	att Ile	651
gtt Val 170	gat Asp	ggc Gly	aac Asn	gga Gly 175	aaa Lys	atc Ile	tgg Trp	tgg Trp	caa Gln 180	aac Asn	tca Ser	tgc Cys	aaa Lys	atc Ile 185	gac Asp	699
aaa Lys	tct Ser	aag Lys	cca Pro 190	tgc Cys	aca Thr	aaa Lys	gcg Ala	cca Pro 195	acg Thr	gct Ala	ctt Leu	act Thr	ctc Leu	tac Tyr 200	aac Asn	747
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gat Asp	tta Leu	act Thr	tgc Cys 285	ggc Gly	ccc Pro	ggt Gly	cat His	ggc Gly 290	atc Ile	agc Ser	att Ile	gga Gly	agc Ser	ttg Leu	ggg Gly	1035
gat Asp	gac Asp	aat Asn 300	tcc Ser	aaa Lys	gct Ala	tat Tyr	gta Val 305	tcg Ser	gga Gly	att Ile	aat Asn 310	gtg Val	gat Asp	ggt Gly	gct Ala	1083
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Lys	Thr	Asp	Asp	Thr	Gln	Ala	Phe	Lys	Lys	Ala	Trp	Lys	Lys	Ala	Cys
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Ser	Pro	Asn	Thr	Asp	Gly	Ile	His	Ile	Val	Ala	Thr	Lys	Asn	Ile	Arg
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Asp	Gly	Ser	Gln	Asn	Val	Gln	Ile	Asn	Asp	Leu	Thr	Cys	Gly	Pro	Gly
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His	Gly	Ile	Ser	Ile	Gly	Ser	Leu	Gly	Asp	Asp	Asn	Ser	Lys	Ala	Tyr
		290					295					300			
Val	Ser	Gly	Ile	Asn	Val	Asp	Gly	Ala	Thr	Leu	Ser	Glu	Thr	Asp	Asn
305				310						315					320
Gly	Val	Arg	Ile	Lys	Thr	Tyr	Gln	Gly	Gly	Ser	Gly	Thr	Ala	Lys	Asn
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Pro

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Gly Gly Leu Glu Thr Val Lys Val Lys Leu Pro Ala Val Ile Ser Ala	
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gac ttg cgg ctc aat gag ccg cgg tac gct act ctg ccc aat atc atg	143
Asp Leu Arg Leu Asn Glu Pro Arg Tyr Ala Thr Leu Pro Asn Ile Met	
35 40 45	
aag gcc aag aag aag ccc atc aaa aag ctc aca gcc aca gat gtc ggt	191
Lys Ala Lys Lys Lys Pro Ile Lys Lys Leu Thr Ala Thr Asp Val Gly	
50 55 60	
gtg gac ttg gcg cca cgt caa caa gtg ttg agc gta gaa gac ccg ccc	239
Val Asp Leu Ala Pro Arg Gln Gln Val Leu Ser Val Glu Asp Pro Pro	
65 70 75	
acc aga cag gct ggt tcc att gtg cct gat gtc gac act ctc atc acc	287
Thr Arg Gln Ala Gly Ser Ile Val Pro Asp Val Asp Thr Leu Ile Thr	
80 85 90 95	
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Lys Leu Lys Glu Lys Gly His Leu	
100	

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Ala Lys Lys Lys Pro Ile Lys Lys Leu Thr Ala Thr Asp Val Gly Val  
50 55 60  
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aaa tcc tct ggt tcg ggt ttt cag tcc cat cag gag ttt ctc tat ggt 95  
Lys Ser Ser Gly Ser Gly Phe Gln Ser His Gln Glu Phe Leu Tyr Gly  
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